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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=11; day=25; hr=8; min=29; sec=34; ms=74;]

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Application No: 10511384

Version No: 4.0

Input Set:**Output Set:****Started:** 2008-10-31 15:17:06.780**Finished:** 2008-10-31 15:17:08.975**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 195 ms**Total Warnings:** 218**Total Errors:** 0**No. of SeqIDs Defined:** 226**Actual SeqID Count:** 226

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Input Set:

Output Set:

Started: 2008-10-31 15:17:06.780
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Total Warnings: 218
Total Errors: 0
No. of SeqIDs Defined: 226
Actual SeqID Count: 226

Error code

Error Description

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<140> 10511384

<141> 2008-10-31

<150> CU 2002/0076

<151> 2002-04-15

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<170> PatentIn version 3.4

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Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln

35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu

50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro

85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Glu Ile Glu Pro Glu

100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys

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Pro Arg Arg

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<212> DNA

<213> Homo Sapiens

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gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180


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aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
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          20             25            30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
      35             40            45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
      50             55            60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
      65             70            75            80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
          85             90            95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Ala Ile Ala Pro Ala
      100            105            110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
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<210> 22
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 atgcgatgcg ggggctgctg caatgacgag ggctggagt gtgtgcccac tgaggagtcc 300
 aacatcacca tgcagattat ggcaatcgca cctgcacaag gccagcacat aggagagatg 360
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<210> 23
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 <212> PRT
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Arg	Leu	Ser	Ile	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Lys	Ala	Asn	Thr	Thr
		35					40					45			
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro
	50					55				60					
Asn	Asn	Gln	Ser	Gly	Ser	Glu	Gln	Arg	Val	Glu	Val	Thr	Glu	Cys	Ser
65					70					75				80	
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			85						90					95	
Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Phe	Tyr	Arg	Glu	Thr	Asp	Leu	Ala	Ser
		100						105					110		
Val	Ile	Tyr	Val	Tyr	Val	Gln	Asp	Tyr	Arg	Ser	Pro	Phe	Ile	Ala	Ser
		115					120						125		
Val	Ser	Asp	Gln	His	Gly	Val	Val	Tyr	Ile	Thr	Glu	Asn	Lys	Asn	Lys
	130					135					140				
Thr	Val	Val	Ile	Pro	Cys	Leu	Gly	Ser	Ile	Ser	Asn	Leu	Asn	Val	Ser
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Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile		
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Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr		
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260	265	270
Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe		
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 <212> DNA
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tggcttttggc ccaataatca gagtggcagt gagcaaaggg tggaggtgac tgagtgcagc	240
gatggcctct tctgtaagac actcacaatt ccaaaagtga tcggaaatga cactggagcc	300
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aacaaaaaca aaactgtggt gattccatgt ctcgggtcca tttcaaactt caacgtgtca	480
ctttgtgcaa gataccaga aaagagattt gttcctgatg gtaacagaat ttctggggac	540
agcaagaag gctttactat tcccagctac atgatcagct atgctggcat ggtcttctgt	600
gaagcaaaaa ttaatgatga aagttaccag tctattatgt acatagttgt cgttgtaggg	660

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aagcttgtct	taaattgtac	agcaagaact	gaactaaatg	tggggattga	cttcaactgg	780
gaataccctt	cttgaagca	tcagcataag	aaacttgtaa	accgagacct	aaaaaccag	840
tctgggagtg	agatgaagaa	atttttgagc	accttaacta	tagatggtgt	aaccggagt	900
gaccaaggat	tgtacacctg	tgcagcatcc	agtgggctga	tga		943

Ala Lys Val Glu Ala Phe Phe Ile Ile Glu Gly Ala Gln Glu Lys Thr
1 5 10 15

Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp
50 55 60

Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp
100 105 110

Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys
145 150 155 160

Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	Phe	Cys	Lys	Phe	165	170	175
Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Ser	Lys	Arg	Asn	Glu	Phe	Val	Pro	180	185	190
Tyr	Lys	Thr	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	Asp	Tyr	Val	Gly	195	200	205
Ala	Ile	Pro	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	Ile	Thr	Ser	Ser	210	215	220
Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	Ser	Leu	Ser	Asp	225	230	235
Val	Glu	Glu	Glu	Glu	Ala	Pro	Glu	Asp	Leu	Tyr	Lys	Asp	Phe	Leu	Thr	245	250	255
Leu	Glu	His	Leu	Ile	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Lys	Gly	Met	Glu	260	265	270
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Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp
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Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr
545 550 555 560

Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser
565 570 575

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